BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

FIG. 1A

```
                                        1
                                       met ala gln trp glu met leu gln
ACTGCAACCCTAATCAGAGCCCAA               ATG GCG CAG TGG GAA ATG CTG CAG

     10                                                  20
asn leu asp ser pro phe gln asp gln leu his gln leu tyr ser
AAT CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG CTT TAC TCG

                                   30
his ser leu leu pro val asp ile arg gln tyr leu ala val trp
CAC AGC CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC TGG

     40                                                  50
ile glu asp gln asn trp gln glu ala ala leu gly ser asp asp
ATT GAA GAC CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT

                                   60
ser lys ala thr met leu phe phe his phe leu asp gln leu asn
TCC AAG GCT ACC ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC

     70                                                  80
tyr glu cys gly arg cys ser gln asp pro glu ser leu leu leu
TAT GAG TGT GGC CGT TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG

                                   90
gln his asn leu arg lys phe cys arg asp ile gln pro phe ser
CAG CAC AAT TTG CGG AAA TTC TGC CGG GAC ATT CAG CCC TTT TCC

    100                                                 110
gln asp pro thr gln leu ala glu met ile phe asn leu leu leu
CAG GAT CCT ACC CAG TTG GCT GAG ATG ATC TTT AAC CTC CTT CTG

                                  120
glu glu lys arg ile leu ile gln ala gln arg ala gln leu glu
GAA GAA AAA AGA ATT TTG ATC CAG GCT CAG AGG GCC CAA TTG GAA

    130                                                 140
gln gly glu pro val leu glu thr pro val glu ser gln gln his
CAA GGA GAG CCA GTT CTC GAA ACA CCT GTG GAG AGC CAG CAA CAT

                                  150
glu ile glu ser arg ile leu asp leu arg ala met met glu lys
GAG ATT GAA TCC CGG ATC CTG GAT TTA AGG GCT ATG ATG GAG AAG

    160                                                 170
leu val lys ser ile ser gln leu lys asp gln gln asp val phe
CTG GTA AAA TCC ATC AGC CAA CTG AAA GAC CAG CAG GAT GTC TTC

                                  180
```

Session Name: rb

FIG. 1B

```
cys phe arg tyr lys ile gln ala lys gly lys thr pro ser leu
TGC TTC CGA TAT AAG ATC CAG GCC AAA GGG AAG ACA CCC TCT CTG

    190                                             200
asp pro his gln thr lys glu gln lys ile leu gln glu thr leu
GAC CCC CAT CAG ACC AAA GAG CAG AAG ATT CTG CAG GAA ACT CTC

                        210
asn glu leu asp lys arg arg lys glu val leu asp ala ser lys
AAT GAA CTG GAC AAA AGG AGA AAG GAG GTG CTG GAT GCC TCC AAA

    220                                             230
ala leu leu gly arg leu thr thr leu ile glu leu leu leu pro
GCA CTG CTA GGC CGA TTA ACT ACC CTA ATC GAG CTA CTG CTG CCA

                        240
lys leu glu glu trp lys ala gln gln gln lys ala cys ile arg
AAG TTG GAG GAG TGG AAG GCC CAG CAG CAA AAA GCC TGC ATC AGA

    250                                             260
ala pro ile asp his gly leu glu gln leu glu thr trp phe thr
GCT CCC ATT GAC CAC GGG TTG GAA CAG CTG GAG ACA TGG TTC ACA

                        270
ala gly ala lys leu leu phe his leu arg gln leu leu lys glu
GCT GGA GCA AAG CTG TTG TTT CAC CTG AGG CAG CTG CTG AAG GAG

    280                                             290
leu lys gly leu ser cys leu val ser tyr gln asp asp pro leu
CTG AAG GGA CTG AGT TGC CTG GTT AGC TAT CAG GAT GAC CCT CTG

                        300
thr lys gly val asp leu arg asn ala gln val thr glu leu leu
ACC AAA GGG GTG GAC CTA CGC AAC GCC CAG GTC ACA GAG TTG CTA

    310                                             320
gln arg leu leu his arg ala phe val val glu thr gln pro cys
CAG CGT CTG CTC CAC AGA GCC TTT GTG GTA GAA ACC CAG CCC TGC

                        330
met pro gln thr pro his arg pro leu ile leu lys thr gly ser
ATG CCC CAA ACT CCC CAT CGA CCC CTC ATC CTC AAG ACT GGC AGC

    340                                             350
lys phe thr val arg thr arg leu leu val arg leu gln glu gly
AAG TTC ACC GTC CGA ACA AGG CTG CTG GTG AGA CTC CAG GAA GGC

                        360
asn glu ser leu thr val glu val ser ile asp arg asn pro pro
AAT GAG TCA CTG ACT GTG GAA GTC TCC ATT GAC AGG AAT CCT CCT

    370                                             380
gln leu gln gly phe arg lys phe asn ile leu thr ser asn gln
CAA TTA CAA GGC TTC CGG AAG TTC AAC ATT CTG ACT TCA AAC CAG

                        390
lys thr leu thr pro glu lys gly gln ser gln gly leu ile trp
```

FIG.1C

Session Name: rb

```
AAA ACT TTG ACC CCC GAG AAG GGG CAG AGT CAG GGT TTG ATT TGG

    400                                             410
asp phe gly tyr leu thr leu val glu gln arg ser gly gly ser
GAC TTT GGT TAC CTG ACT CTG GTG GAG CAA CGT TCA GGT GGT TCA

                        420
gly lys gly ser asn lys gly pro leu gly val thr glu glu leu
GGA AAG GGC AGC AAT AAG GGG CCA CTA GGT GTG ACA GAG GAA CTG

    430                                             440
his ile ile ser phe thr val lys tyr thr tyr gln gly leu lys
CAC ATC ATC AGC TTC ACG GTC AAA TAT ACC TAC CAG GGT CTG AAG

                        450
gln glu leu lys thr asp thr leu pro val val ile ile ser asn
CAG GAG CTG AAA ACG GAC ACC CTC CCT GTG GTG ATT ATT TCC AAC

    460                                             470
met asn gln leu ser ile ala trp ala ser val leu trp phe asn
ATG AAC CAG CTC TCA ATT GCC TGG GCT TCA GTT CTC TGG TTC AAT

                        480
leu leu ser pro asn leu gln asn gln gln phe phe ser asn pro
TTG CTC AGC CCA AAC CTT CAG AAC CAG CAG TTC TTC TCC AAC CCC

    490                                             500
pro lys ala pro trp ser leu leu gly pro ala leu ser trp gln
CCC AAG GCC CCC TGG AGC TTG CTG GGC CCT GCT CTC AGT TGG CAG

                        510
phe ser ser tyr val gly arg gly leu asn ser asp gln leu ser
TTC TCC TCC TAT GTT GGC CGA GGC CTC AAC TCA GAC CAG CTG AGC

    520                                             530
met leu arg asn lys leu phe gly gln asn cys arg thr glu asp
ATG CTG AGA AAC AAG CTG TTC GGG CAG AAC TGT AGG ACT GAG GAT

                        540
pro leu leu ser trp ala asp phe thr lys arg glu ser pro pro
CCA TTA TTG TCC TGG GCT GAC TTC ACT AAG CGA GAG AGC CCT CCT

    550                                             560
gly lys leu pro phe trp thr trp leu asp lys ile leu glu leu
GGC AAG TTA CCA TTC TGG ACA TGG CTG GAC AAA ATT CTG GAG TTG

                        570
val his asp his leu lys asp leu trp asn asp gly arg ile met
GTA CAT GAC CAC CTG AAG GAT CTC TGG AAT GAT GGA CGC ATC ATG

    580                                             590
gly phe val ser arg ser gln glu arg arg leu leu lys lys thr
GGC TTT GTG AGT CGG AGC CAG GAG CGC CGG CTG CTG AAG AAG ACC

                        600
met ser gly thr phe leu leu arg phe ser glu ser ser glu gly
ATG TCT GGC ACC TTT CTA CTG CGC TTC AGT GAA TCG TCA GAA GGG
```

Session Name: rb

FIG.1D

```
    610                                                 620
gly ile thr cys ser trp val glu his gln asp asp asp lys val
GGC ATT ACC TGC TCC TGG GTG GAG CAC CAG GAT GAT GAC AAG GTG

                        630
leu ile tyr ser val gln pro tyr thr lys glu val leu gln ser
CTC ATC TAC TCT GTG CAA CCG TAC ACG AAG GAG GTG CTG CAG TCA

    640                                                 650
leu pro leu thr glu ile ile arg his tyr gln leu leu thr glu
CTC CCG CTG ACT GAA ATC ATC CGC CAT TAC CAG TTG CTC ACT GAG

                        660
glu asn ile pro glu asn pro leu arg phe leu tyr pro arg ile
GAG AAT ATA CCT GAA AAC CCA CTG CGC TTC CTC TAT CCC CGA ATC

    670                                                 680
pro arg asp glu ala phe gly cys tyr tyr gln glu lys val asn
CCC CGG GAT GAA GCT TTT GGG TGC TAC TAC CAG GAG AAA GTT AAT

                        690
leu gln glu arg arg lys tyr leu lys his arg leu ile val val
CTC CAG GAA CGG AGG AAA TAC CTG AAA CAC AGG CTC ATT GTG GTC

    700                                                 710
ser asn arg gln val asp glu leu gln gln pro leu glu leu lys
TCT AAT AGA CAG GTG GAT GAA CTG CAA CAA CCG CTG GAG CTT AAG

                        720
pro glu pro glu leu glu ser leu glu leu glu leu gly leu val
CCA GAG CCA GAG CTG GAG TCA TTA GAG CTG GAA CTA GGG CTG GTG

    730                                                 740
pro glu pro glu leu ser leu asp leu glu pro leu leu lys ala
CCA GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA

                        750
gly leu asp leu gly pro glu leu glu ser val leu glu ser thr
GGG CTG GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT

    760                                                 770
leu glu pro val ile glu pro thr leu cys met val ser gln thr
CTG GAG CCT GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA

                        780
val pro glu pro asp gln gly pro val ser gln pro val pro glu
GTG CCA GAG CCA GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG

    790                                                 800
pro asp leu pro cys asp leu arg his leu asn thr glu pro met
CCA GAT TTG CCC TGT GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG

                        810
glu ile phe arg asn cys val lys ile glu glu ile met pro asn
GAA ATC TTC AGA AAC TGT GTA AAG ATT GAA GAA ATC ATG CCG AAT
```

FIG. 1E

Session Name: rb

```
    820                                                 830
gly asp pro leu leu ala gly gln asn thr val asp glu val tyr
GGT GAC CCA CTG TTG GCT GGC CAG AAC ACC GTG GAT GAG GTT TAC

                        840
val ser arg pro ser his phe tyr thr asp gly pro leu met pro
GTC TCC CGC CCC AGC CAC TTC TAC ACT GAT GGA CCC TTG ATG CCT

    850 851
ser asp phe AM
TCT GAC TTC TAG GAACCACATTTCCTCTGTTCTTTTCATATCTCTTTGCCCTTCCTA

CTCCTCATAGCATGATATTGTTCTCCAAGGATGGGAATCAGGCATGTGTCCCTTCCAAGC

TGTGTTAACTGTTCAAACTCAGGCCTGTGTGACTCCATTGGGGTGAGAGGTGAAAGCATA

ACATGGGTACAGAGGGGACAACAATGAATCAGAACAGATGCTGAGCCATAGGTCTAAATA

GGATCCTGGAGGCTGCCTGCTGTGCTGGGAGGTATAGGGGTCCTGGGGGCAGGCCAGGGC

AGTTGACAGGTACTTGGAGGGCTCAGGGCAGTGGCTTCTTTCCAGTATGGAAGGATTTCA

ACATTTTAATAGTTGGTTAGGCTAAACTGGTGCATACTGGCATTGGCCTTGGTGGGGAGC

ACAGACACAGGATAGGACTCCATTTCTTTCTTCCATTCCTTCATGTCTAGGATAACTTGC

TTTCTTCTTTCCTTTACTCCTGGCTCAAGCCCTGAATTTCTTCTTTTCCTGCAGGGGTTG

AGAGCTTTCTGCCTTAGCCTACCATGTGAAACTCTACCCTGAAGAAAGGGATGGATAGGA

AGTAGACCTCTTTTTCTTACCAGTCTCCTCCCCTACTCTGCCCCCTAAGCTGGCTGTACC

TGTTCCTCCCCCATAAAATGATCCTGCCAATCTAAAAAAAAAA
```

FIG. 2A

```
ATTAAACCTCTCGCCGAGCCCCTCCGCAGACTCTGCGCCGGAAAGTTTCATTTGCTGTATGCCA

TCCTCGAGAGCTGTCTAGGTTAACGTTCGCACTCTGTGTATATAACCTCGACAGTCTTGGCACC

TAACGTGCTGTGCGTAGCTGCTCCTTTGGTTGAATCCCCAGGCCCTTGTTGGGGCACAAGGTGG

     Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu
CAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC TCA AAA TTC CTG

 Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg
 GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC ATG GAA ATC AGA

 Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala
 CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG GAG CAC GCT GCC

 Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln
 AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC CTC CTG TCA CAG

 Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu
 CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT AAC TTC TTG CTA

 Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln
 CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG GAT AAT TTT CAG

 Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu
 GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC TGT CTG AAG GAA

 Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser
 GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT CAG GCT CAG TCG

 Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp
 GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG AAA GAG CTT GAC

 Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu
 AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT ATA GAG CAT GAA

 Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys
 ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC TTC AAA TGC AAA

 Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp
 ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG GCA AAG AGT GAT

 Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr L u Met Leu Asp
 CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT TTA ATG CTT GAC

Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val
AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG TTG CTG AAT GTC
```

FIG. 2B

```
Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp
ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA CTA GTG GAG TGG

Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys
AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG CCC AAT GCT TGC

Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln
TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG GAG AGT CTG CAG

Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr
CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG GAA CAG AAA TAC

Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp
ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA GTG TTA TGG GAC

Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val
CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC TCG TTT GTG GTG

Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu
GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG CCG CTG GTC TTG

Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu
AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG TTG GTG AAA TTG

Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp
CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA TTT GAT AAA GAT

Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu
GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG TTC AAC ATT TTG

Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser
GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC ACC AAT GGC AGT

Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala
CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA CAG AAA AAT GCT

Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His
GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT GAA GAG CTT CAC

Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp
TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT TTG GTA ATT GAC

Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln
CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC AAC GTC AGC CAG

Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala
CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC ATG CTG GTG GCG

Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp
GAA CCC AGG AAT CTG TCC TTC TTC CTG ACT CCA CCA TGT GCA CGA TGG
```

FIG. 2C

```
Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys
GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT TCT GTC ACC AAA

Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu
AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA GAG AAG CTT CTT

Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys
GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG ACG AGG TTT TGT

Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu
AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG CTT TGG ATT GAA

Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp
AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT CTC TGG AAT GAT

Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu
GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG CGT GCC CTG TTG

Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser
AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC AGT GAG AGC TCC

Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly
CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG TCC CAG AAC GGA

Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu
GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG AAG AAA GAA CTT

Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala
TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC AAA GTC ATG GCT

Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile
GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG TAT CCA AAT ATT

Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala
GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG CCA AAG GAA GCA

Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys
CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT GGA TAT ATC AAG

Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr
ACT GAG TTG ATT TCT GTG TCT GAA GTT CAC CCT TCT AGA CTT CAG ACC

Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser
ACA GAC AAC CTG CTC CCC ATG TCT CCT GAG GAG TTT GAC GAG GTG TCT

Arg Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val
CGG ATA GTG GGC TCT GTA GAA TTC GAC AGT ATG ATG AAC ACA GTA TAG

AGCATGAATTTTTTTCATCTTCTCTGGCGACAGTTTTCCTTCTCATCTGTGATTCCCTCCTGCT
```

FIG. 2D

ACTCTGTTCCTTCACATCCTGTGTTTCTAGGGAAATGAAAGAAAGGCCAGCAAATTCGCTGCA

ACCTGTTGATAGCAAGTGAATTTTTCTCTAACTCAGAAACATCAGTTACTCTGAAGGGCATCA

TGCATCTTACTGAAGGTAAAATTGAAAGGCATTCTCTGAAGAGTGGGTTTCACAAGTGAAAAA

CATCCAGATACACCCAAAGTATCAGGACGAGAATGAGGGTCCTTTGGGAAAGGAGAAGTTAAG

CAACATCTAGCAAATGTTATGCATAAAGTCAGTGCCCAACTGTTATAGGTTGTTGGATAAATC

AGTGGTTATTTAGGGAACTGCTTGACGTAGGAACGGTAAATTTCTGTGGGAGAATTCTTACAT

GTTTTCTTTGCTTTAAGTGTAACTGGCAGTTTTCCATTGGTTTACCTGTGAAATAGTTCAAAG

CCAAGTTTATATACAATTATATCAGTCCTCTTTCAAAGGTAGCCATCATGGATCTGGTAGGGG

GAAAATGTGTATTTTATTACATCTTTCACATTGGCTATTTAAAGACAAAGACAAATTCTGTTT

CTTGAGAAGAGAAATTTCCAAATTCACAAGTTGTGTTTGATATCCAAAGCTGAATACATTCTG

CTTTCATCTTGGTCACATACAATTATTTTTACAGTTCTCCCAAGGGAGTTAGGCTATTCACAA

CCACTCATTCAAAAGTTGAAATTAACCATAGATGTAGATAAACTCAGAAATTTAATTCATGTT

TCTTAAATGGGCTACTTTGTCCTTTTTGTTATTAGGGTGGTATTTAGTCTATTAGCCACAAAA

TTGGGAAAGGAGTAGAAAAAGCAGTAACTGACAACTTGAATAATACACCAGAGATAATATGAG

AATCAGATCATTTCAAAACTCATTTCCTATGTAACTGCATTGAGAACTGCATATGTTTCGCTG

ATATATGTGTTTTTCACATTTGCGAATGGTTCCATTCTCTCTCCTGTACTTTTTCCAGACACT

TTTTTGAGTGGATGATGTTTCGTGAAGTATACTGTATTTTTACCTTTTTCCTTCCTTATCACT

GACACAAAAAGTAGATTAAGAGATGGGTTTGACAAGGTTCTTCCCTTTTACATACTGCTGTCT

ATGTGGCTGTATCTTGTTTTTCCACTACTGCTACCACAACTATATTATCATGCAAATGCTGTA

TTCTTCTTTGGTGGAGATAAAGATTTCTTGAGTTTTGTTTTAAAATTAAAGCTAAAGTATCTG

TATTGCATTAAATATAATATCGACACAGTGCTTTCCGTGGCACTGCATACAATCTGAGGCCTC

CTCTCTCAGTTTTTATATAGATGGCGAGAACCTAAGTTTCAGTTGATTTTACAATTGAAATGA

CTAAAAAACAAAGAAGACAACATTAAAAACAATATTGTTTCTA

FIG. 3A

```
ATTAAACCTCTCGCCGAGCCCCTCCGCAGACTCTGCGCCGGAAAGTTTCATTTGCTGTATGCC
ATCCTCGAGAGCTGTCTAGGTTAACGTTCGCACTCTGTGTATATAACCTCGACAGTCTTGGCA
CCTAACGTGCTGTGCGTAGCTGCTCCTTTGGTTGAATCCCCAGGCCCTTGTTGGGGCACAAGG

          Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe
TGGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC TCA AAA TTC

Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile
CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC ATG GAA ATC

Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala
AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG GAG CAC GCT

Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser
GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC CTC CTG TCA

Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu
CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT AAC TTC TTG

Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe
CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG GAT AAT TTT

Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys
CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC TGT CTG AAG

Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln
GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT CAG GCT CAG

Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu
TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG AAA GAG CTT

Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His
GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT ATA GAG CAT

Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys
GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC TTC AAA TGC

Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser
AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG GCA AAG AGT

Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu
GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT TTA ATG CTT

Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn
GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG TTG CTG AAT

Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu
GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA CTA GTG GAG
```

FIG. 3B

```
Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala
TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG CCC AAT GCT

Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu
TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG GAG AGT CTG

Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys
CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG GAA CAG AAA

Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp
TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA GTG TTA TGG

Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val
GAC CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC TCG TTT GTG

Val Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val
GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG CCG CTG GTC

Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys
TTG AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG TTG GTG AAA

Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys
TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA TTT GAT AAA

Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile
GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG TTC AAC ATT

Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly
TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC ACC AAT GGC

Ser Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn
AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA CAG AAA AAT

Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu
GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT GAA GAG CTT

His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile
CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT TTG GTA ATT

Asp Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser
GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC AAC GTC AGC

Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val
CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC ATG CTG GTG

Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg
GCG GAA CCC AGG AAT CTG TCC TTC TTC CTG ACT CCA CCA TGT GCA CGA

Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr
TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT TCT GTC ACC
```

FIG. 3C

```
Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu
AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA GAG AAG CTT

Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe
CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG ACG AGG TTT

Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Il
TGT AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG CTT TGG ATT

Glu Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn
GAA AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT CTC TGG AAT

Asp Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu
GAT GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG CGT GCC CTG

Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser
TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC AGT GAG AGC

Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn
TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG TCC CAG AAC

Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu
GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG AAG AAA GAA

Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met
CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC AAA GTC ATG

Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn
GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG TAT CCA AAT

Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu
ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG CCA AAG GAA

Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile
GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT GGA TAT ATC

Lys Thr Glu Leu Ile Ser Val Ser Glu Val

AAG ACT GAG TTG ATT TCT GTG TCT GAA GTG TAAGTGAACACAGAAGAGTGACA

TGTTTACAAACCTCAAGCCAGCCTTGCTCCTGGCTGGGGCCTGTTGAAGATGCTTGTATTTTA

CTTTTCCATTGTAATTGCTATCGCCATCACAGCTGAACTTGTTGAGATCCCCGTGTTACTGCC

TATCAGCATTTTACTACTTTAAAAAAAAAAAAAAAAGCCAAAAACCAAATTTGTATTTAAGGT

ATATAAATTTTCCCAAAACTGATACCCTTTGAAAAAGTATAAATAAAATGAGCAAAAGTTGAA
```

FIG. 4

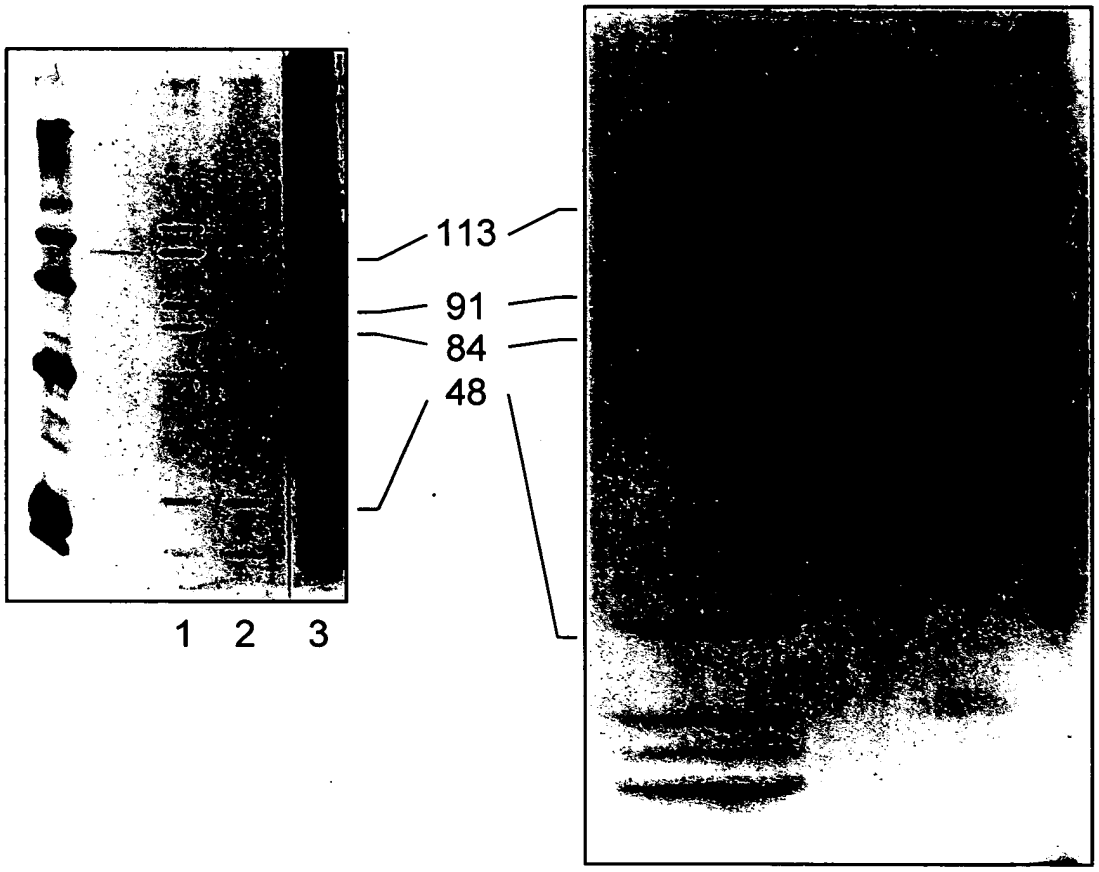

FIG. 5A

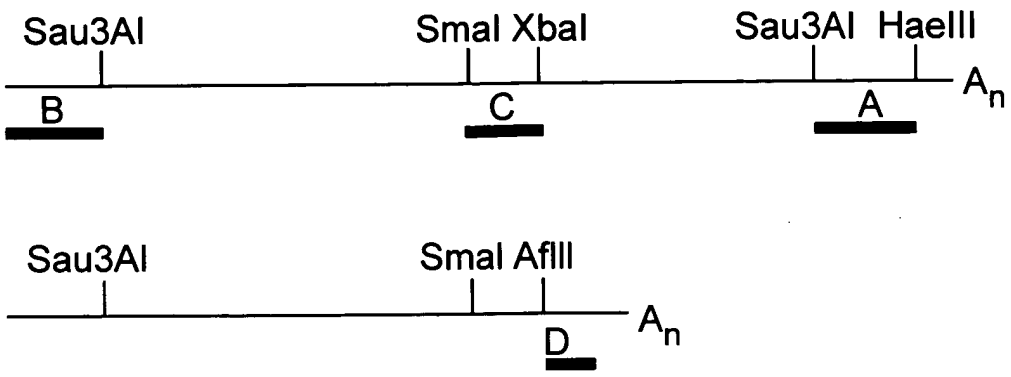

FIG. 5B

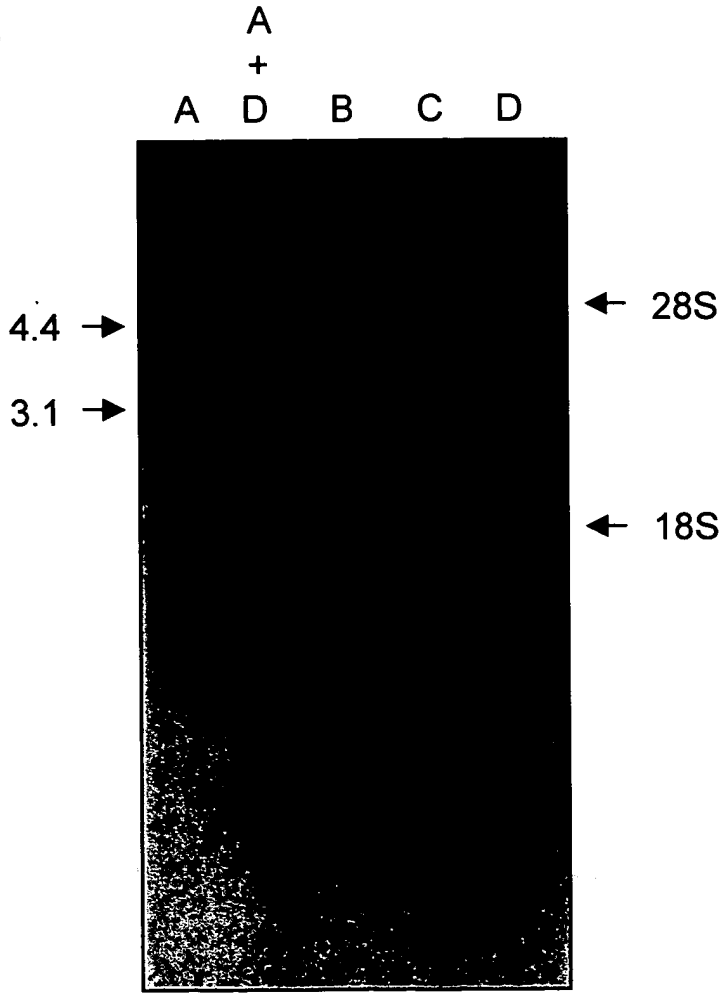

FIG. 6

```
  1 MSQWYELQQLDSKFLEQVHQLYDDSFPMEIRQYLAQWLEKQDWEHAANDV

 51 SFATIRFHDLLSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPIQ

101 MSMIIYSCLKEERKILENAQRFNQAQSGNIQSTVMLDKQKELDSKVRNVK

151 DKVMCIEHEIKSLEDLQDEYDFKCKTLQNREHETNGVAKSDQKQEQLLLK

201 KMYLMLDNKRKEVVHKIIELLNVTELTQNALINDELVEWKRRQQSACIGG

251 PPNACLDQLQQVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLFQQ

301 LIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYNLKVK

351 VLFDKDVNERNTVKGFRKFNILGTHEKVMNMEESTNGSLAAEFRHLQLKE

401 QKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVVISNV

451 SQLPSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTK
          127
501 RGLNVDQLNMLGEKLLGPNASPDGLIPWTRFCKENINDKNFPFWLWIESI
          119
551 LELIKKHLLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGA

601 ITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRNYKVMAAENIPE
                                                  113a
651 NPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDGPKGTGYIKTELISVSE
          113b
701 VHPSRLQTTDNLLPMSPEEPDEVSRIVGSVEFDSMMNTV
    ↑
    last amino acid of 84 kd
```

FIG. 7A

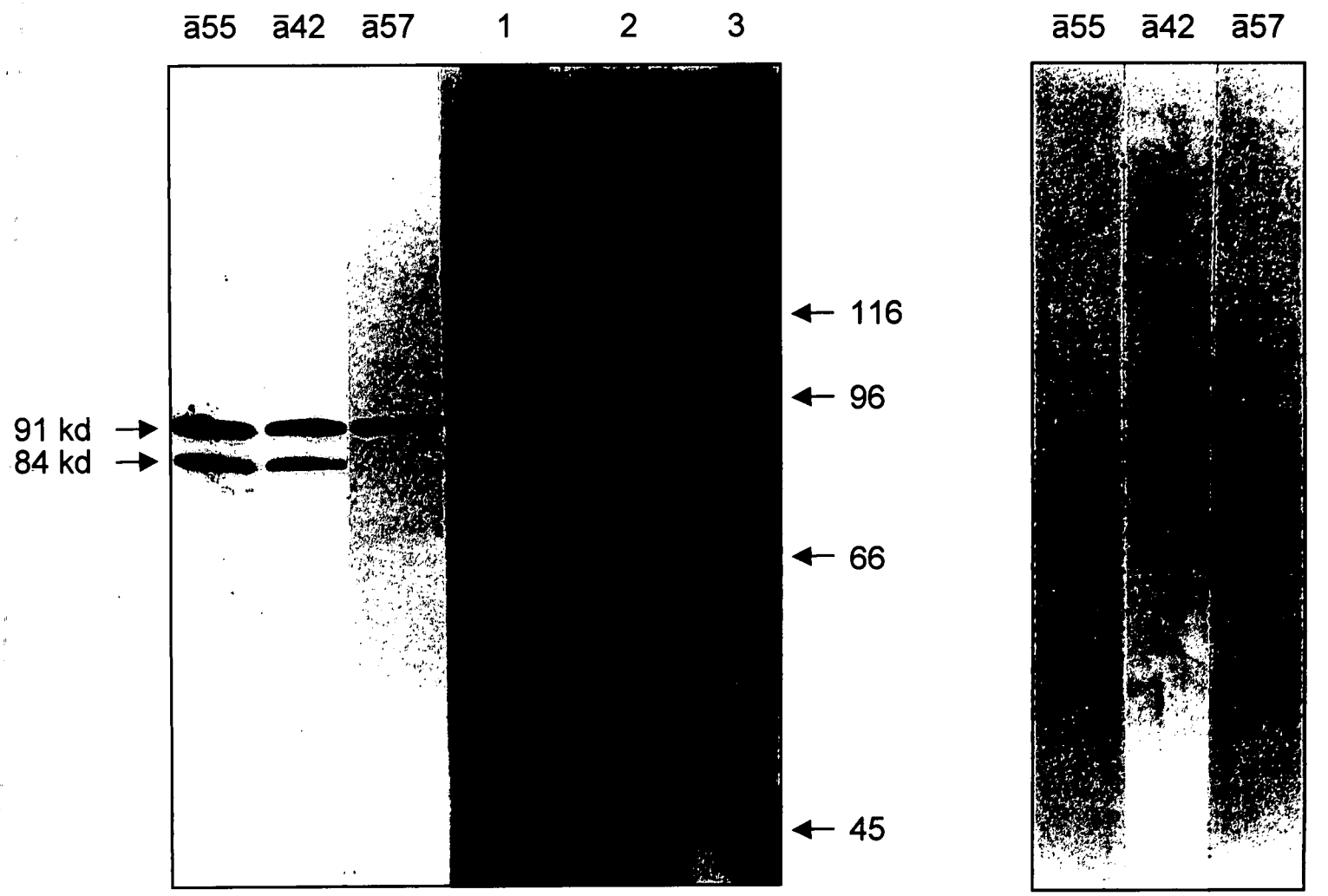

FIG. 7B

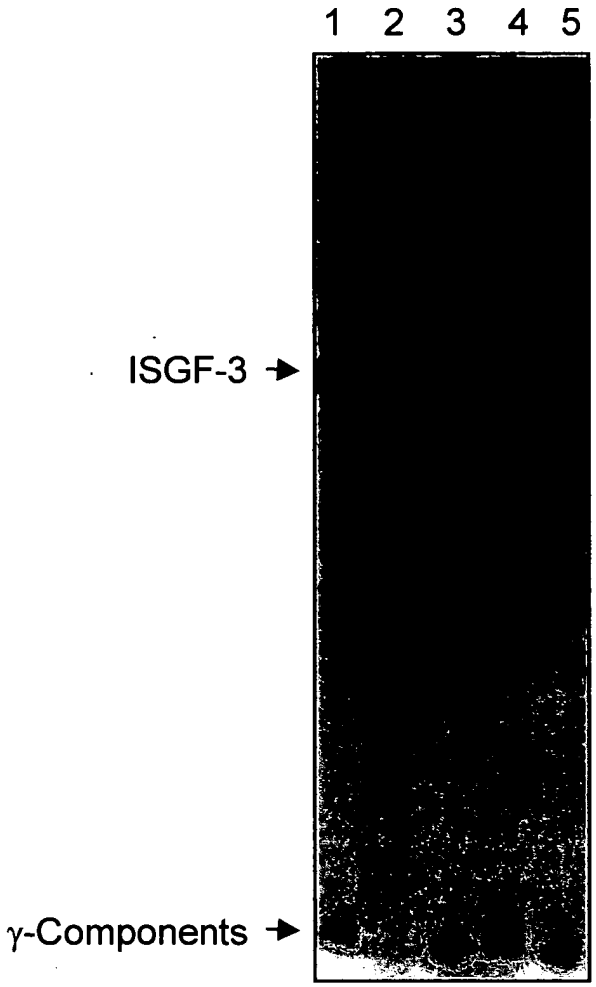

FIG. 8A

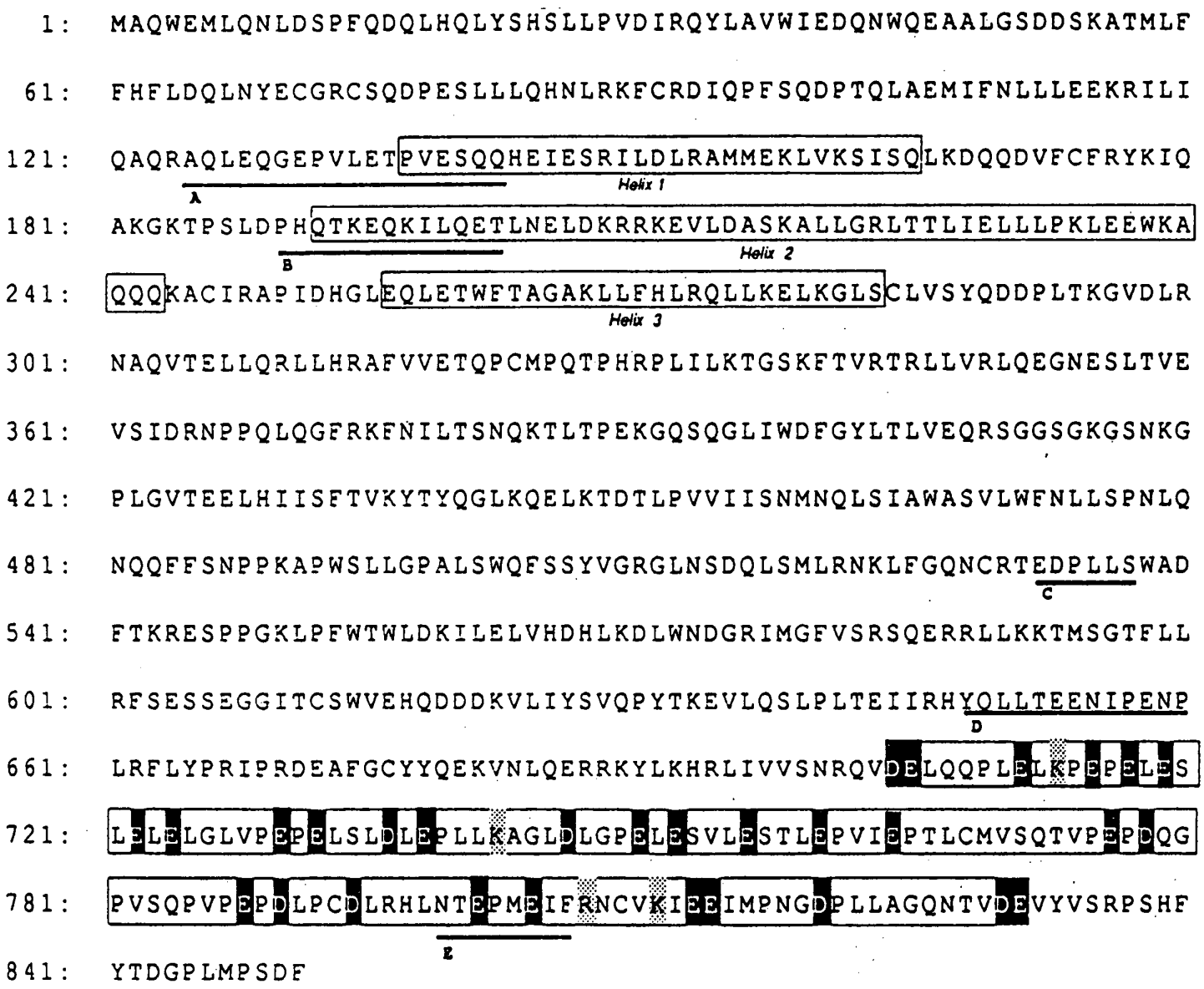

FIG. 8B

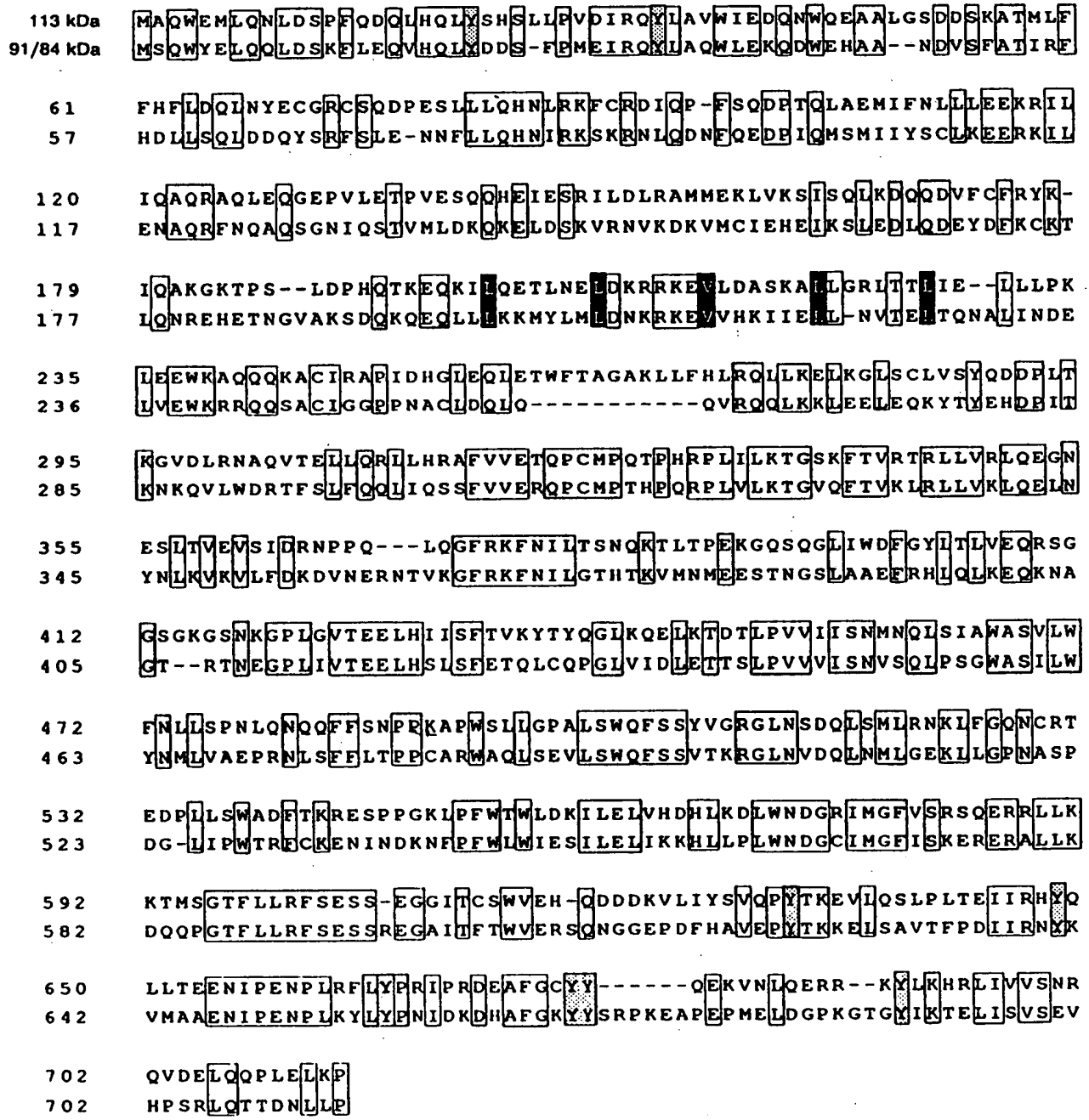

FIG. 9A

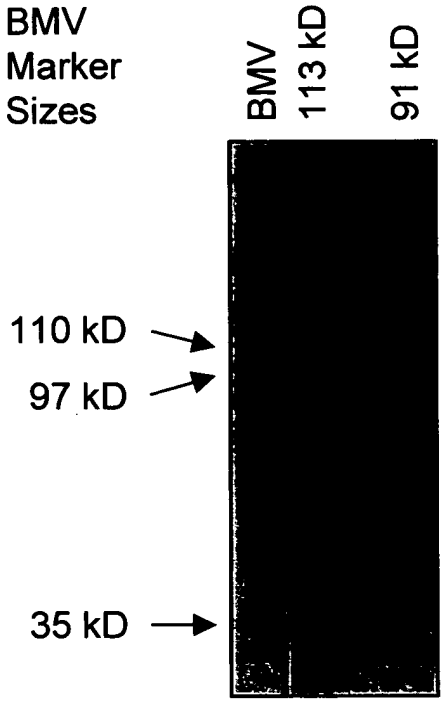

FIG. 9B

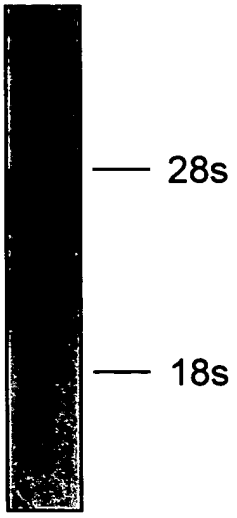

FIG. 10A

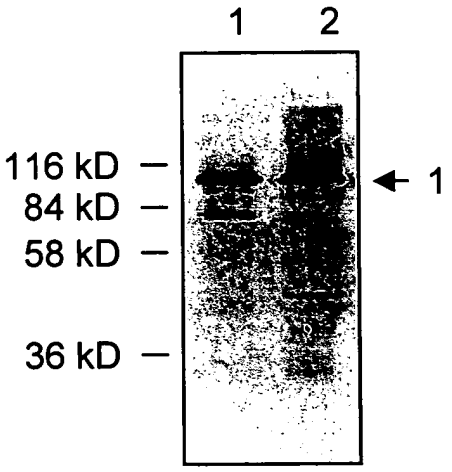

FIG. 10B

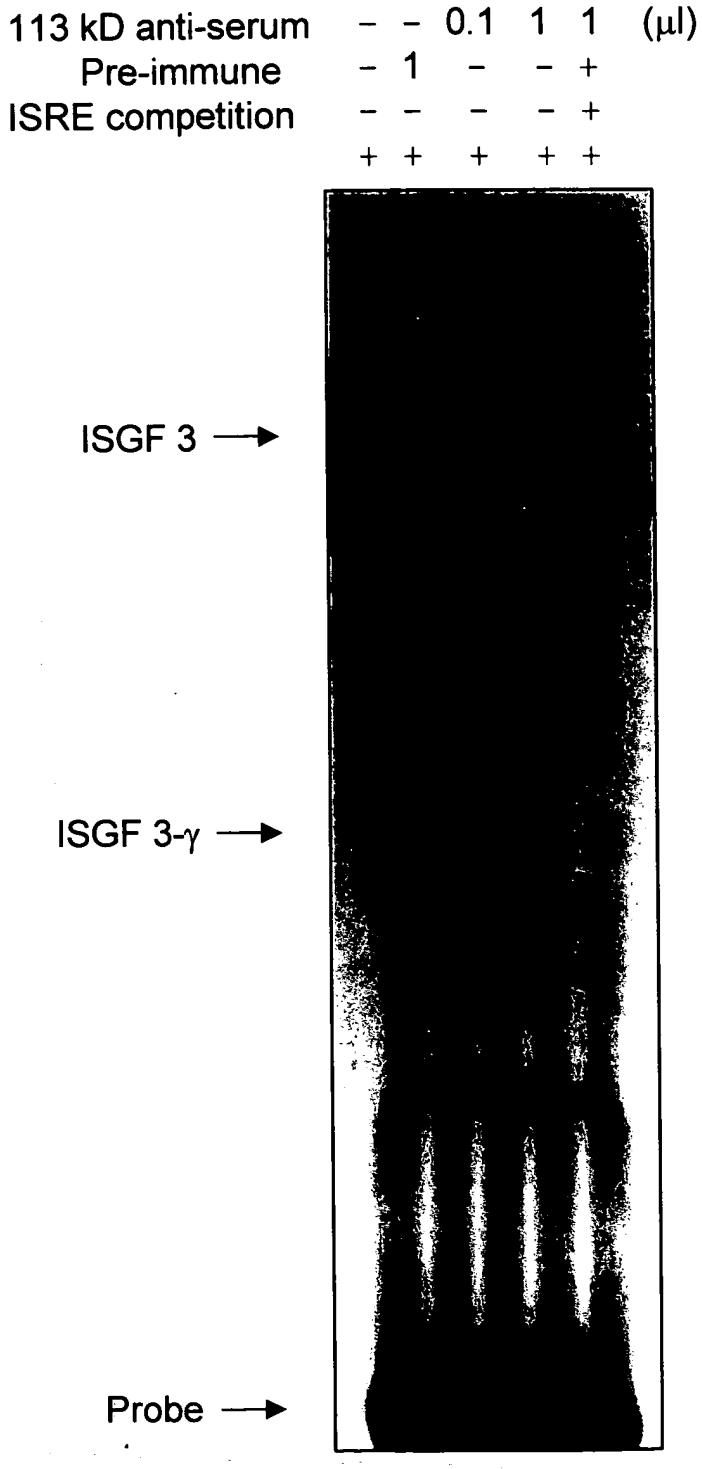

FIG. 11

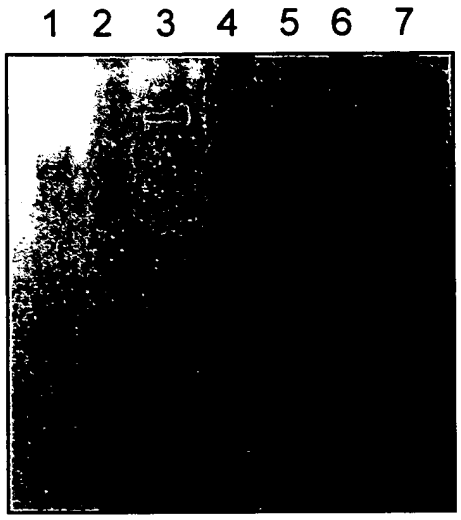

FIG. 12

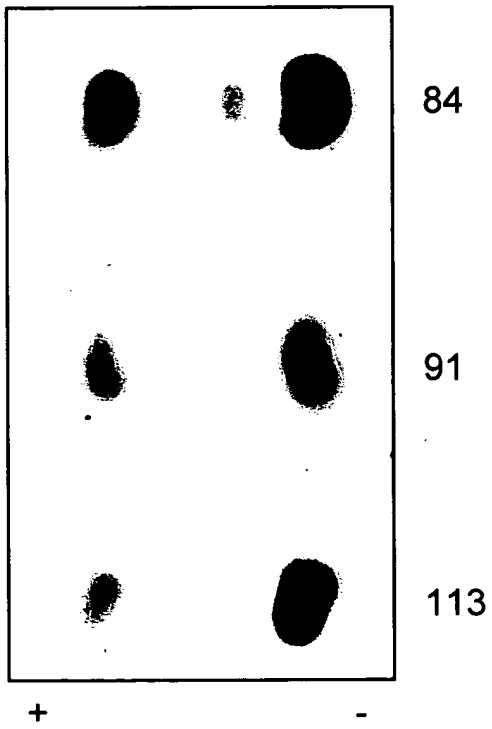

FIG. 13A

Mouse 91kD (protein)

Amino acid sequence (deduced)

```
  1  MSQWFELQQL DSKFLEQVHQ LYDDSFPMEI RQYLAQWLEK QDWEHAAYDV

 51  SFATIRFHDL LSQLDDQYSR FSLENNFLLQ HNIRKSKRNL QDNFQEDPVQ

101  MSMIIYNCLK EERKILENAQ RFNQAQEGNI QNTVMLDKQK ELDSKVRNVK

151  DQVMCIEQEI KTLEELQDEY DFKCKTSQNR EGEANGVAKS DQKQEQLLLH

201  KMFLMLDNKR KEIIHKIREL LNSIELTQNT LINDELVEWK RRQQSACIGG

251  PPNACLDQLQ TWFTIVAETL QQIRQQLKKL EELEQKFTYE PDPITKNKQV

301  LSDRTFLLFQ QLIQSSFVVE RQPCMPTHPQ RPLVLKTGVQ FTVKSRLLVK

351  LQESNLLTKV KCHFDKDVNE KNTVKGFRKF NILGTHTKVM NMEESTNGSL

401  AAELRHLQLK EQKNAGNRTN EGPLIVTEEL HSLSFETQLC QPGLVIDLET

451  TSLPVVVISN VSQLPSGWAS ILWYNMLVTE PRNLSFFLNP PCAWWSQLSE

501  VLSWQFSSVT KRGLNADQLS MLGEKLLGPN AGPDGLIPWT RFCKENINDK

551  NFSFWPWIDT ILELIKNDLL CLWNDGCIMG FISKERERAL LKDQQPGTFL

601  LRFSESSREG AITFTWVERS QNGGEPDFHA VEPYTKKELS AVTFPDIIRN

651  YKVMAAENIP ENPLKYLYPN IDKDHAFGKY YSRPKEAPEP MELDDPKRTG

701  YIKTELISVS EVHPSRLQTT DNLLPMSPEE FDEMSRIVGP EFDSMMSTV
```

FIG. 13B

Mouse 91kD (protein) DNA sequence

```
   1  caggatgtca cagtggttcg agcttcagca gctggactcc aagttcctgg
  51  agcaggtcca ccagctgtac gatgacagtt tccccatgga aatcagacag
 101  tacctggccc agtggctgga aaagcaagac tgggagcacg ctgcctatga
 151  tgtctcgttt gcgaccatcc gcttccatga cctcctctca cagctggacg
 201  accagtacag ccgcttttct ctggagaata atttcttgtt gcagcacaac
 251  atacggaaaa gcaagcgtaa tctccaggat aacttccaag aagatcccgt
 301  acagatgtcc atgatcatct acaactgtct gaaggaagaa aggaagattt
 351  tggaaaatgc ccaaagattt aatcaggccc aggagggaaa tattcagaac
 401  actgtgatgt tagataaaca gaaggagctg gacagtaaag tcagaaatgt
 451  gaaggatcaa gtcatgtgca tagagcagga aatcaagacc ctagaagaat
 501  tacaagatga atatgacttt aaatgcaaaa cctctcagaa cagagaaggt
 551  gaagccaatg gtgtggcgaa gagcgaccaa aaacaggaac agctgctgct
 601  ccacaagatg tttttaatgc ttgacaataa gagaaaggag ataattcaca
```

FIG. 13C

651 aaatcagaga gttgctgaat tccatcgagc tcactcagaa cactctgatt

701 aatgacgagc tcgtggagtg gaagcgaagg cagcagagcg cctgcatcgg

751 gggaccgccc aacgcctgcc tggatcagct gcaaacgtgg ttcaccattg

801 ttgcagagac cctgcagcag atccgtcagc agcttaaaaa gctggaggag

851 ttggaacaga aattcaccta tgagcccgac cctattacaa aaaacaagca

901 ggtgttgtca gatcgaacct tcctcctctt ccagcagctc attcagagct

951 ccttcgtggt agaacgacag ccgtgcatgc ccactcaccc gcagaggccc

1001 ctggtcttga agactggggt acagttcact gtcaagtcga gactgttggt

1051 gaaattgcaa gagtcgaatc tattaacgaa agtgaaatgt cactttgaca

1101 aagatgtgaa cgagaaaaac acagttaaag gatttcggaa gttcaacatc

1151 ttgggtacgc acacaaaagt gatgaacatg gaagaatcca ccaacggaag

1201 tctggcagct gagctccgac acctgcaact gaaggaacag aaaaacgctg

1251 ggaacagaac taatgagggg cctctcattg tcaccgaaga acttcactct

1301 cttagctttg aaacccagtt gtgccagcca ggcttggtga ttgacctgga

1351 gaccacctct cttcctgtcg tggtgatctc caacgtcagc cagctcccca

FIG. 13D

1401 gtggctgggc gtctatcctg tggtacaaca tgctggtgac agagcccagg

1451 aatctctcct tcttcctgaa ccccccgtgc gcgtggtggt cccagctctc

1501 agaggtgttg agttggcagt tttcatcagt caccaagaga ggtctgaacg

1551 cagaccagct gagcatgctg ggagagaagc tgctgggccc taatgctggc

1601 cctgatggtc ttattccatg gacaaggttt tgtaaggaaa atattaatga

1651 taaaaatttc tccttctggc cttggattga caccatccta gagctcatta

1701 agaacgacct gctgtgcctc tggaatgatg ggtgcattat gggcttcatc

1751 agcaaggagc gagaacgcgc totgctcaag gaccagcagc cagggacgtt

1801 cctgcttaga ttcagtgaga gctcccggga aggggccatc acattcacat

1851 gggtggaacg gtcccagaac ggaggtgaac ctgacttcca tgccgtggag

1901 ccctacacga aaaaagaact ttcagctgtt actttcccag atattattcg

1951 caactacaaa gtcatggctg ccgagaacat accagagaat cccctgaagt

2001 atctgtaccc caatattgac aaagaccacg cctttgggaa gtattattcc

2051 agaccaaagg aagcaccaga accgatggag cttgacgacc ctaagcgaac

2101 tggatacatc aagactgagt tgatttctgt gtctgaagtc caccettcta

2151 gacttcagac cacagacaac ctgcttccca tgtctccaga ggagtttgat

2201 gagatgtccc ggatagtggg ccccgaattt gacagtatga tgagcacagt

2251 ataaacacga atttctctct ggcgaca

FIG. 14A

13sf1(protein)

Amino acid sequence of 13sf1

1 MSQWNQVQQL EIKFLEQVDQ FYDDNFPMEI RHLLAQWIET QDWEVASNNE

51 TMATILLQNL LIQLDEQLGR VSKEKNLLLI HNLKRIRKVL QGKFHGNPMH

101 VAVVISNCLR EERRILAAAN MPIQGPLEKS LQSSSVSERQ RNVEHKVSAI

151 KNSVQMTEQD TKYLEDLQDE FDYRYKTIQT MDQGDKNSIL VNQEVLTLLQ

201 EMLNSLDFKR KEALSKMTQI VNETDLLMNS MLLEELQDWK KRHRIACIGG

251 PLHNGLDQLQ NCFTLLAESL FQLRQQLEKL QEQSTKMTYE GDPIPAQRAH

301 LLERATFLIY NLFKNSFVVE RHACMPTHPQ RPMVLKTLIQ FTVKLRLLIK

351 LPELNYQVKV KASIDKNVST LSNRRFVLCG THVKAMSSEE SSNGSLSVEL

401 DIATQGDEVQ YWSKGNEGCH MVTEELHSIT FETQICLYGL TINLETSSLP

451 VVMISNVSQL PNAWASIIWY NVSTNDSQNL VFFNNPPSVT LGQLLEVMSW

501 QFSSYVGRGL NSEQLNMLAE KLTVQSNYND GHLTWAKFCK EHLPGKTFTF

551 WTWLEAILDL IKKHILPLWI DGYIMGFVSK EKERLLLKDK MPGTFLLRFS

601 ESHLGGITFT WVDQSENGEV RFHSVEPYNK GRLSALAFAD ILRDYKVIMA

651 ENIPENPLKY LYPDIPKDKA FGKHYSSQPC EVSRPTERGD KGYVPSVFIP

701 ISTIRSDSTE PQSPSDLLPM SPSAYAVLRE NLSPTTIETA MNSPYSAE

FIG. 14B

13sf1(DNA)

DNA sequence of 13sf1

```
   1  tgccactacc tggacggaga gagagagagc agcatgtctc agtggaatca

  51  agtccaacaa ttagaaatca agtttttgga gcaagtagat cagttctatg

 101  atgacaactt tcctatggaa atccggcatc tgctagctca gtggattgag

 151  actcaagact gggaagtagc ttctaacaat gaaactatgg caacaattct

 201  gcttcaaaac ttactaatac aattggatga acagttgggg cgggtttcca

 251  aagaaaaaaa tctgctattg attcacaatc taaagagaat tagaaaagtt

 301  cttcagggca agtttcatgg aaatccaatg catgtagctg tggtaatttc

 351  aaattgctta agggaagaga ggagaatatt ggctgcagcc aacatgccta

 401  tccagggacc tctggagaaa tccttacaga gttcttcagt ttctgaaaga

 451  caaaggaatg tggaacacaa agtgtctgcc attaaaaaca gtgtgcagat

 501  gacagaacaa gataccaaat acttagaaga cctgcaagat gagtttgact

 551  acaggtataa aacaattcag acaatggatc agggtgacaa aaacagtatc

 601  ctggtgaacc aggaagtttt gacactgctg caagaaatgc ttaatagtct

 651  ggacttcaag agaaaggaag cactcagtaa gatgacgcag atagtgaacg

 701  agacagacct gctcatgaac agcatgcttc tagaagagct gcaggactgg

 751  aaaaagcggc acaggattgc ctgcattggt ggcccgctcc acaatgggct

 801  ggaccagctt cagaactgct ttaccctact ggcagagagt cttttccaac

 851  tcagacagca actggagaaa ctacaggagc aatctactaa aatgacctat
```

FIG. 14C

13sf1 (DNA)

901 gaaggggatc ccatccctgc tcaaagagca cacctcctgg aaagagctac

951 cttcctgatc tacaaccttt tcaagaactc atttgtggtc gagcgacacg

1001 catgcatgcc aacgcaccct cagaggccga tggtacttaa aaccctcatt

1051 cagttcactg taaaactgag attactaata aaattgccgg aactaaacta

1101 tcaggtgaaa gtaaaggcgt ccattgacaa gaatgtttca actctaagca

1151 atagaagatt tgtgctttgt ggaactcacg tcaaagctat gtccagtgag

1201 gaatcttcca atgggagcct ctcagtggag ttagacattg caacccaagg

1251 agatgaagtg cagtactgga gtaaaggaaa cgagggctgc cacatggtga

1301 cagaggagtt gcattccata acctttgaga cccagatctg cctctatggc

1351 ctcaccatta acctagagac cagctcatta cctgtcgtga tgatttctaa

1401 tgtcagccaa ctacctaatg catgggcatc catcatttgg tacaatgtat

1451 caactaacga ctcccagaac ttggttttct ttaataaccc tccatctgtc

1501 actttgggcc aactcctgga agtgatgagc tggcaatttt catcctatgt

1551 cggtcgtggc cttaattcag agcagctcaa catgctggca gagaagctca

1601 cagttcagtc taactacaat gatggtcacc tcacctgggc caagttctgc

1651 aaggaacatt tgcctggcaa aacatttacc ttctggactt ggcttgaagc

1701 aatattggac ctaattaaaa aacatattct tcccctctgg attgatgggt

1751 acatcatggg atttgttagt aaagagaagg aacggcttct gctcaaagat

1001 aaaatgcctg ggacattttt gttaagattc agtgagagcc atcttggagg

FIG. 14D

13sf1 (DNA)

1851 gataaccttc acctgggtgg accaatctga aaatggagaa gtgagattcc

1901 actctgtaga accctacaac aaagggagac tgtcggctct ggccttcgct

1951 gacatcctgc gagactacaa ggttatcatg gctgaaaaca tccctgaaaa

2001 ccctctgaag tacctctacc ctgacattcc caaagacaaa gcctttggca

2051 aacactacag ctcccagccg tgcgaagtct caagaccaac cgaacgggga

2101 gacaagggtt acgtcccctc tgtttttatc cccatttcaa caatccgaag

2151 cgattccacg gagccacaat ctccttcaga ccttctcccc atgtctccaa

2201 gtgcatatgc tgtgctgaga gaaaacctga gcccaacgac aattgaaact

2251 gcaatgaatt ccccatattc tgctgaatga cggtgcaaac ggacacttta

2301 aagaaggaag cagatgaaac tggagagtgt tctttaccat agatcacaat

2351 ttatttcttc ggctttgtaa atacc

FIG. 15A

19sf6(DNA)

Amino acid sequence of 19sf6

```
   1  MAQWNQLQQL DTRYLKQLHQ LYSDTFPMEL RQFLAPWIES QDWAYAASKE

  51  SHATLVFHNL LGEIDQQYSR FLQESNVLYQ HNLRRIKQFL QSRYLEKPME

 101  IARIVARCLW EESRLLQTAA TAAQQGGQAN HPTAAVVTEK QQMLEQHLQD

 151  VRKRVQDLEQ KMKVVENLQD DFDFNYKTLK SQGDMQDLNG NNQSVTRQKM

 201  QQLEQMLTAL DQMRRSIVSE LAGLLSAMEY VQKTLTDEEL ADWKRRPEIA

 251  CIGGPPNICL DRLENWITSL AESQLQTRQQ IKKLEELQQK VSYKGDPIVQ

 301  HRPMLEERIV ELFRNLMKSA FVVERQPCMP MHPDRPLVIK TGVQFTTKVR

 351  LLVKFPELNY QLKIKVCIDK DSGDVAALRG SRKFNILGTN TKVMNMEESN

 401  NGSLSAEFKH LTLREQRCGN GGRANCDASL IVTEELHLIT FETEVYHQGL

 451  KIDLETHSLP VVVISNICQM PNAWASILWY NMLTNNPKNV NFFTKPPIGT

 501  WDQVAEVLSW QFSSTTKRGL SIEQLTTLAE KLLGPGVNYS GCQITWAKFC

 551  KENMAGKGFS FWVWLDNIID LVKKYILALW NEGYIMGFIS KERERAILST

 601  KPPGTFLLRF SESSKEGGVT FTWVEKDISG KTQIQSVEPY TKQQLNNMSF

 651  AEIIMGYKIM DATNILVSPL VYLYPDIPKE EAFGKYCRPE SQEHPEADPG

 701  SAAPYLKTKF ICVTPTTCSN TIDLPMSPRT LDSLMQFGNN GEGAEPSAGG

 751  QFESLTFDMD LTSECATSPM
```

FIG. 15B

19sf6(DNA)

Amino acid sequence of 19sf6

```
   1  gccgcgacca gccaggccgg ccagtcgggc tcagcccgga gacagtcgag

  51  acccctgact gcagcaggat ggctcagtgg aaccagctgc agcagctgga

 101  cacacgctac ctgaagcagc tgcaccagct gtacagcgac acgttcccca

 151  tggagctgcg gcagttcctg gcaccttgga ttgagagtca agactgggca

 201  tatgcagcca gcaaagagtc acatgccacg ttggtgtttc ataatctctt

 251  gggtgaaatt gaccagcaat atagccgatt cctgcaagag tccaatgtcc

 301  tctatcagca caaccttcga agaatcaagc agtttctgca gagcaggtat

 351  cttgagaagc caatggaaat tgcccggatc gtggcccgat gcctgtggga

 401  agagtctcgc ctcctccaga cggcagccac ggcagcccag caaggggcc

 451  aggccaacca cccaacagcc gccgtagtga cagagaagca gcagatgttg

 501  gagcagcatc ttcaggatgt ccggaagcga gtgcaggatc tagaacagaa

 551  aatgaaggtg gtggagaacc tccaggacga ctttgatttc aactacaaaa

 601  ccctcaagag ccaaggagac atgcaggatc tgaatggaaa caaccagtct

 651  gtgaccagac agaagatgca gcagctggaa cagatgctca cagccctgga

 701  ccagatgcgg agaagcattg tgagtgagct ggcggggctc ttgtcagcaa

 751  tggagtacgt gcagaagaca ctgactgatg aagagctggc tgactggaag

 801  aggcggccag agatcgcgtg catcggaggc cctcccaaca tctgcctgga

 851  ccgtctggaa aactggataa cttcattagc agaatctcaa cttcagaccc
```

FIG. 15C

19sf6(DNA)

901 gccaacaaat taagaaactg gaggagctgc agcagaaagt gtcctacaag

951 ggcgacccta tcgtgcagca ccggcccatg ctggaggaga ggatcgtgga

1001 gctgttcaga aacttaatga agagtgcctt cgtggtggag cggcagccct

1051 gcatgcccat gcacccggac cggcccttag tcatcaagac tggtgtccag

1101 tttaccacga aagtcaggtt gctggtcaaa tttcctgagt tgaattatca

1151 gcttaaaatt aaagtgtgca ttgataaaga ctctggggat gttgctgccc

1201 tcagagggtc tcggaaattt aacattctgg gcacgaacac aaaagtgatg

1251 aacatggagg agtctaacaa cggcagcctg tctgcagagt tcaagcacct

1301 gacccttagg gagcagagat gtgggaatgg aggccgtgcc aattgtgatg

1351 cctccttgat cgtgactgag gagctgcacc tgatcacctt cgagactgag

1401 gtgtaccacc aaggcctcaa gattgaccta gagacccact ccttgccagt

1451 tgtggtgatc tccaacatct gtcagatgcc aaatgcttgg gcatcaatcc

1501 tgtggtataa catgctgacc aataacccca agaacgtgaa cttcttcact

1551 aagccgccaa ttggaacctg ggaccaagtg gccgaggtgc tcagctggca

1601 gttctcgtcc accaccaagc gagggctgag catcgagcag ctgacaacgc

1651 tggctgagaa gctcctaggg cctggtgtga actactcagg gtgtcagatc

1701 acatgggcta aattctgcaa agaaaacatg gctggcaagg gcttctcctt

1751 ctgggtctgg ctagacaata tcatcgacct tgtgaaaaag tatatcttgg

1801 ccctttggaa tgaagggtac atcatgggtt tcatcagcaa ggagcgggag

FIG. 15D

19sf6(DNA)

1851 cgggccatcc taagcacaaa gccccgggc accttcctac tgcgcttcag

1901 cgagagcagc aaagaaggag gggtcacttt cacttgggtg gaaaaggaca

1951 tcagtggcaa gacccagatc cagtctgtag agccatacac caagcagcag

2001 ctgaacaaca tgtcatttgc tgaaatcatc atgggctata agatcatgga

2051 tgcgaccaac atcctggtgt ctccacttgt ctacctctac cccgacattc

2101 ccaaggagga ggcatttgga aagtactgta ggcccgagag ccaggagcac

2151 cccgaagccg acccaggtag tgctgccccg tacctgaaga ccaagttcat

2201 ctgtgtgaca ccaacgacct gcagcaatac cattgacctg ccgatgtccc

2251 cccgcacttt agattcattg atgcagtttg gaaataacgg tgaaggtgct

2301 gagccctcag caggagggca gtttgagtcg ctcacgtttg acatggatct

2351 gacctcggag tgtgctacct cccccatgtg aggagctgaa accagaagct

2401 gcagagacgt gacttgagac acctgccccg tgctccaccc ctaagcagcc

2451 gaaccccata tcgtctgaaa ctcctaactt tgtggttcca gatttttttt

2501 tttaatttcc tacttctgct atctttgggc aatctgggca ctttttaaaa

2551 gagagaaatg agtgagtgtg ggtgataaac tgttatgtaa agaggagaga

2601 cctctgagtc tggggatggg gctgagagca gaagggaggc aaaggggaac

2651 acctcctgtc ctgcccgcct gccctccttt ttcagcagct cgggggttgg

2701 ttgttagaca agtgcctcct ggtgcccatg gctacctgtt gccccactct

2751 gtgagctgat accccattct gggaactcct ggctctgcac tttcaacctt

FIG. 15E

19sf6(DNA)

2001 gctaatatcc acatagaagc taggactaag cccaggaggt tcctctttaa

2051 attaaaaaaa aaaaaaaaa

FIG. 16A

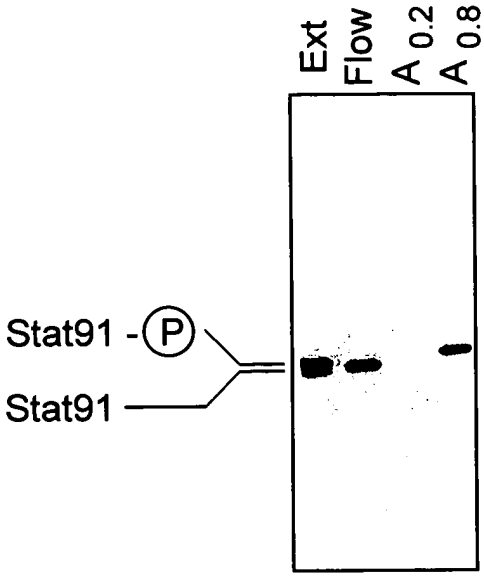

FIG. 16B

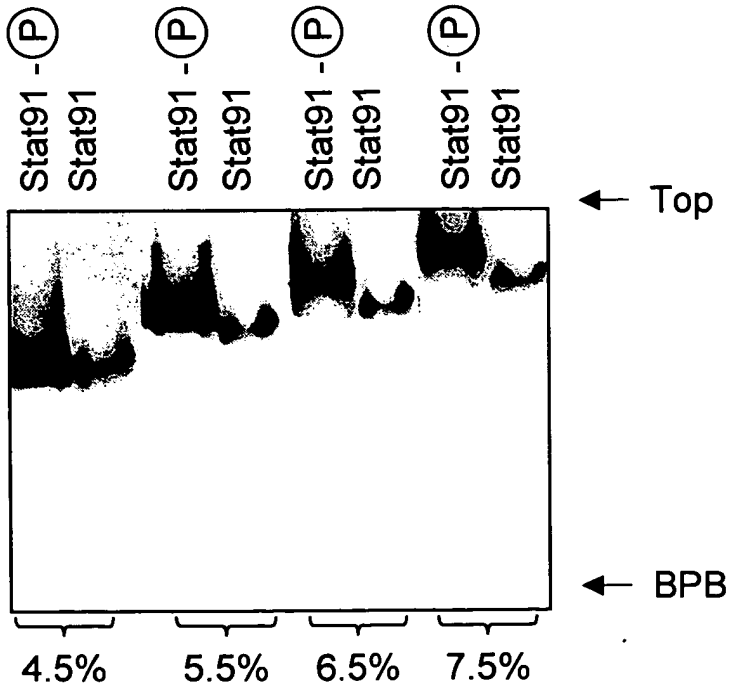

FIG.16C

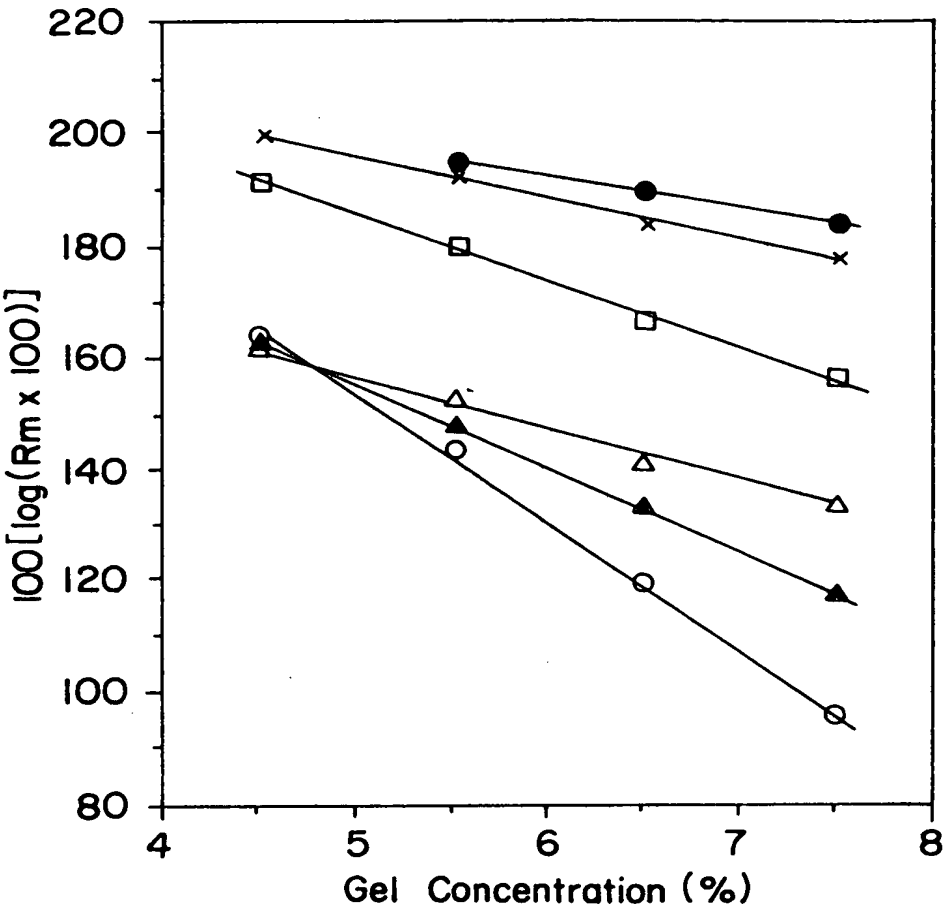

FIG.16D

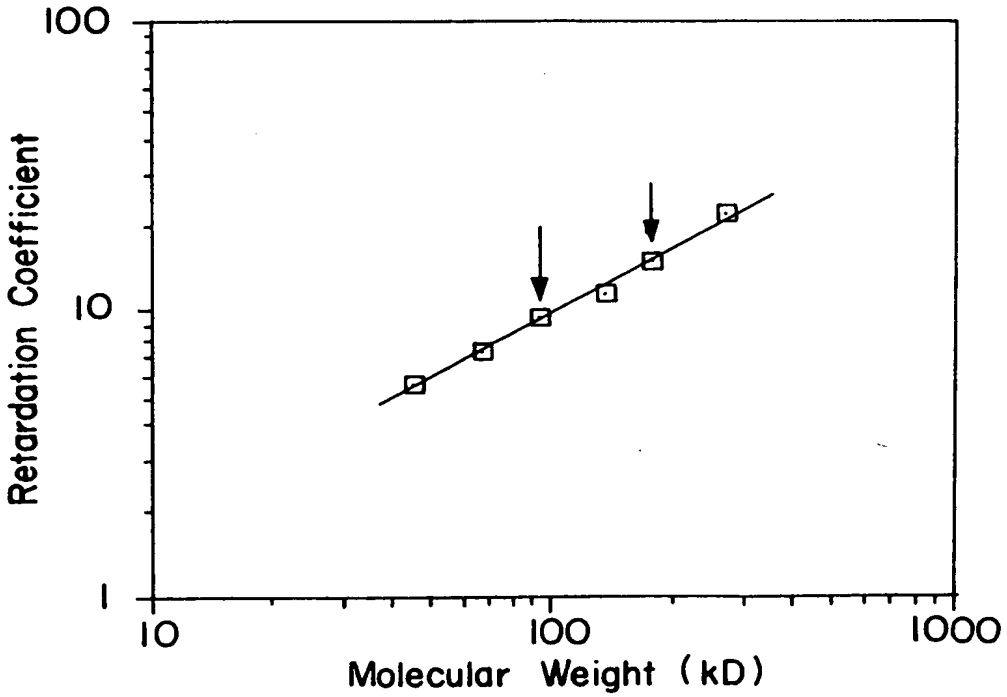

FIG. 17A

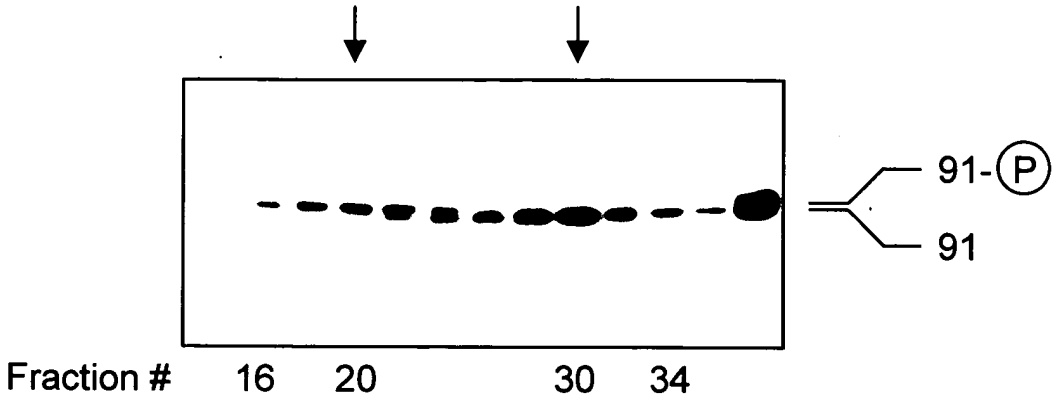

FIG. 17B

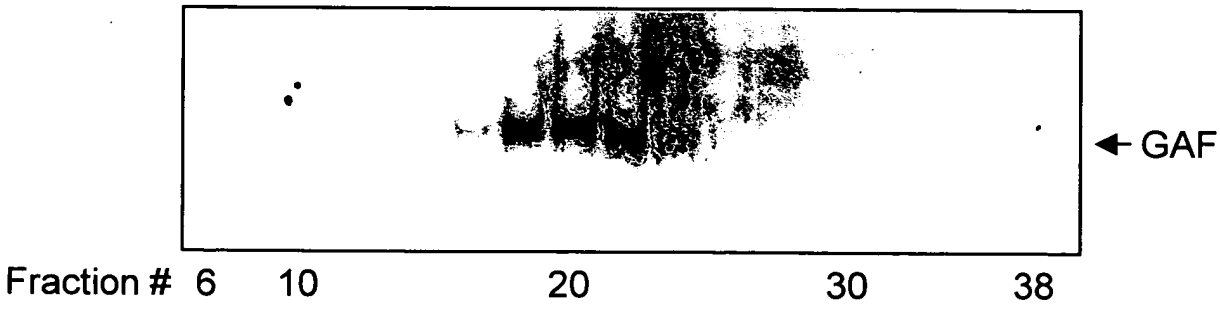

FIG.17C

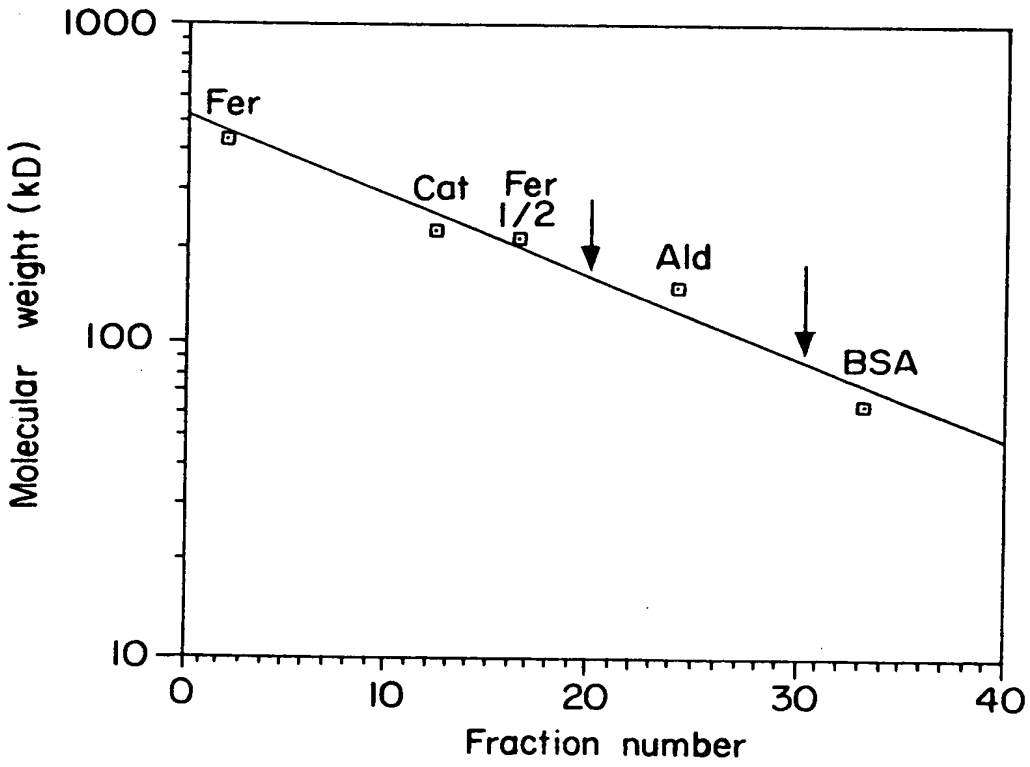

FIG. 18A

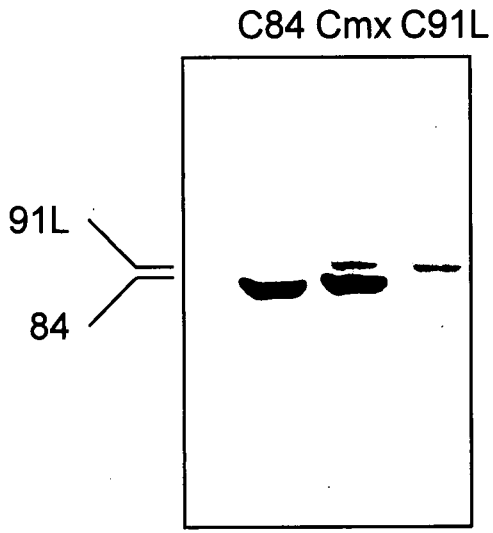

FIG. 18B

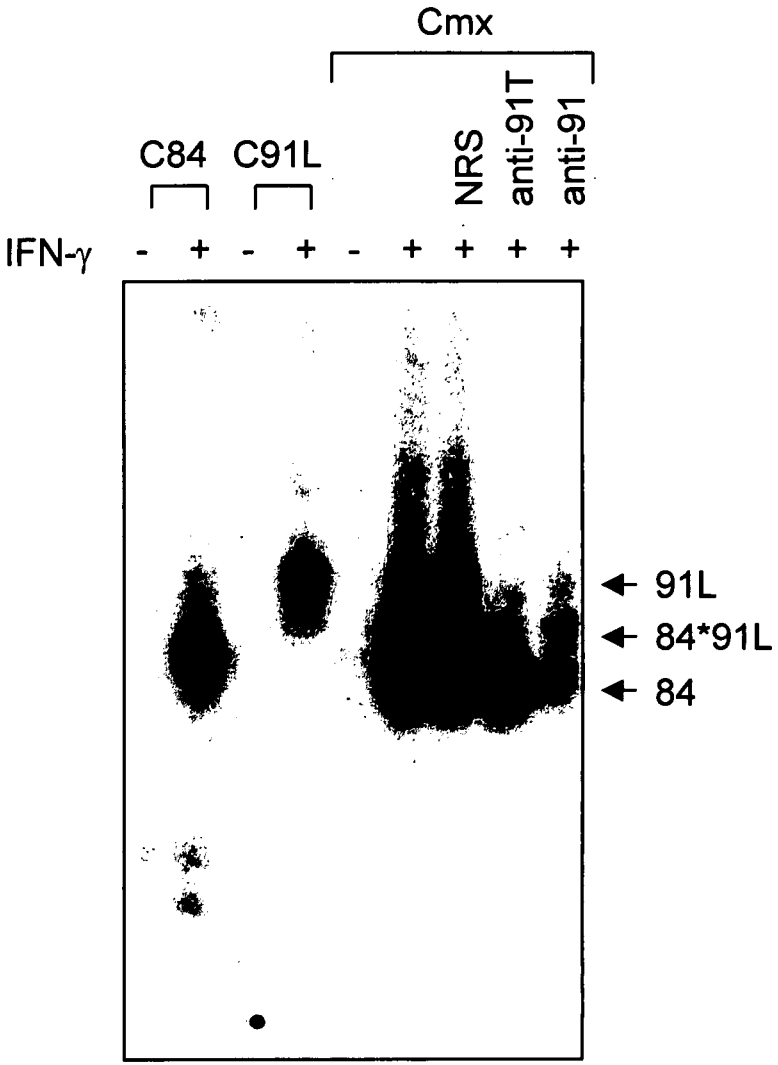

FIG. 19

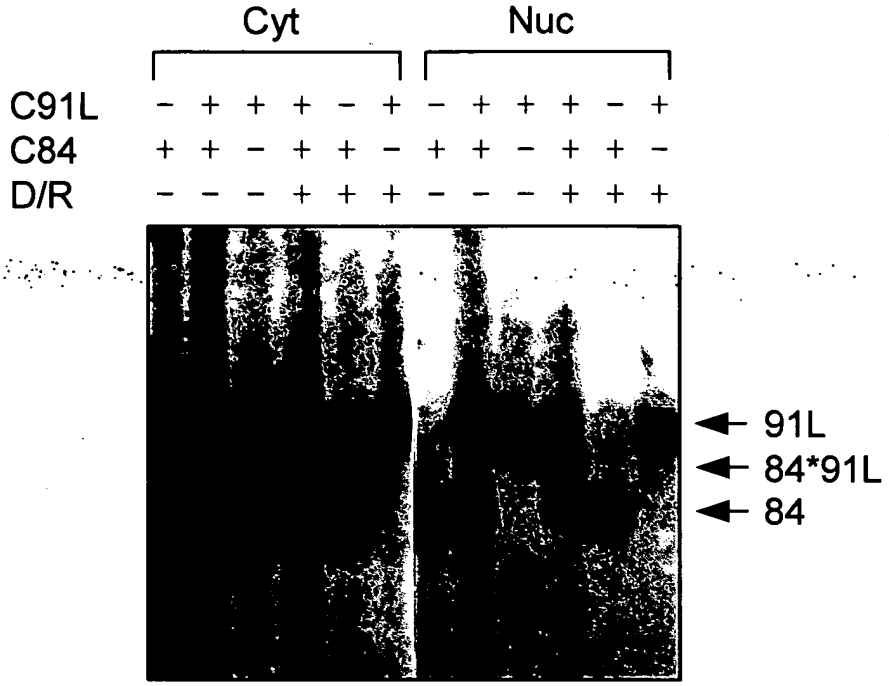

FIG. 20

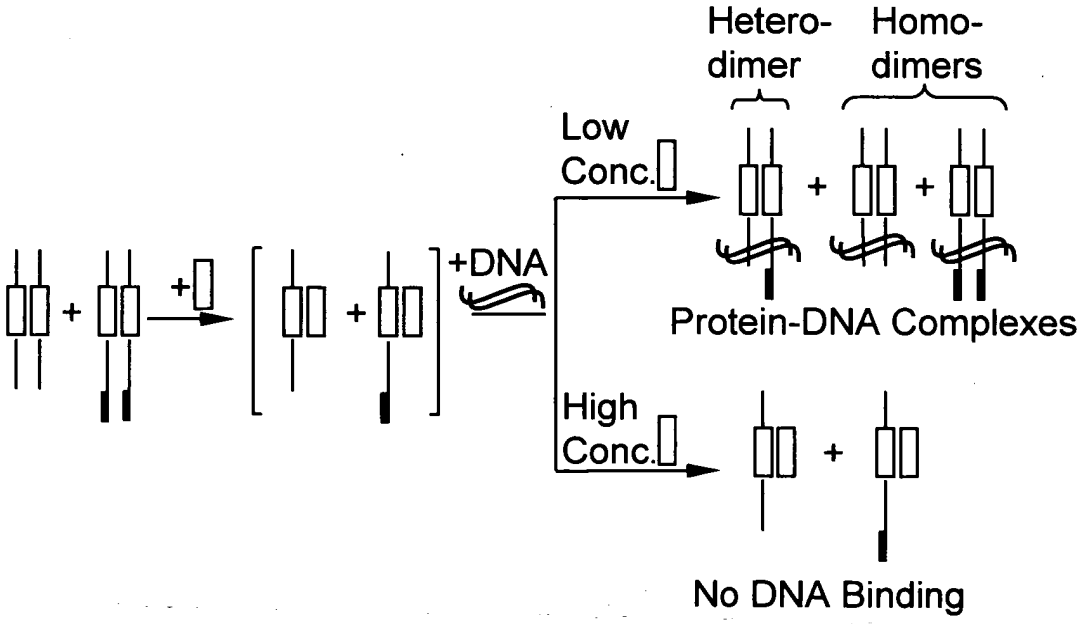

FIG. 21

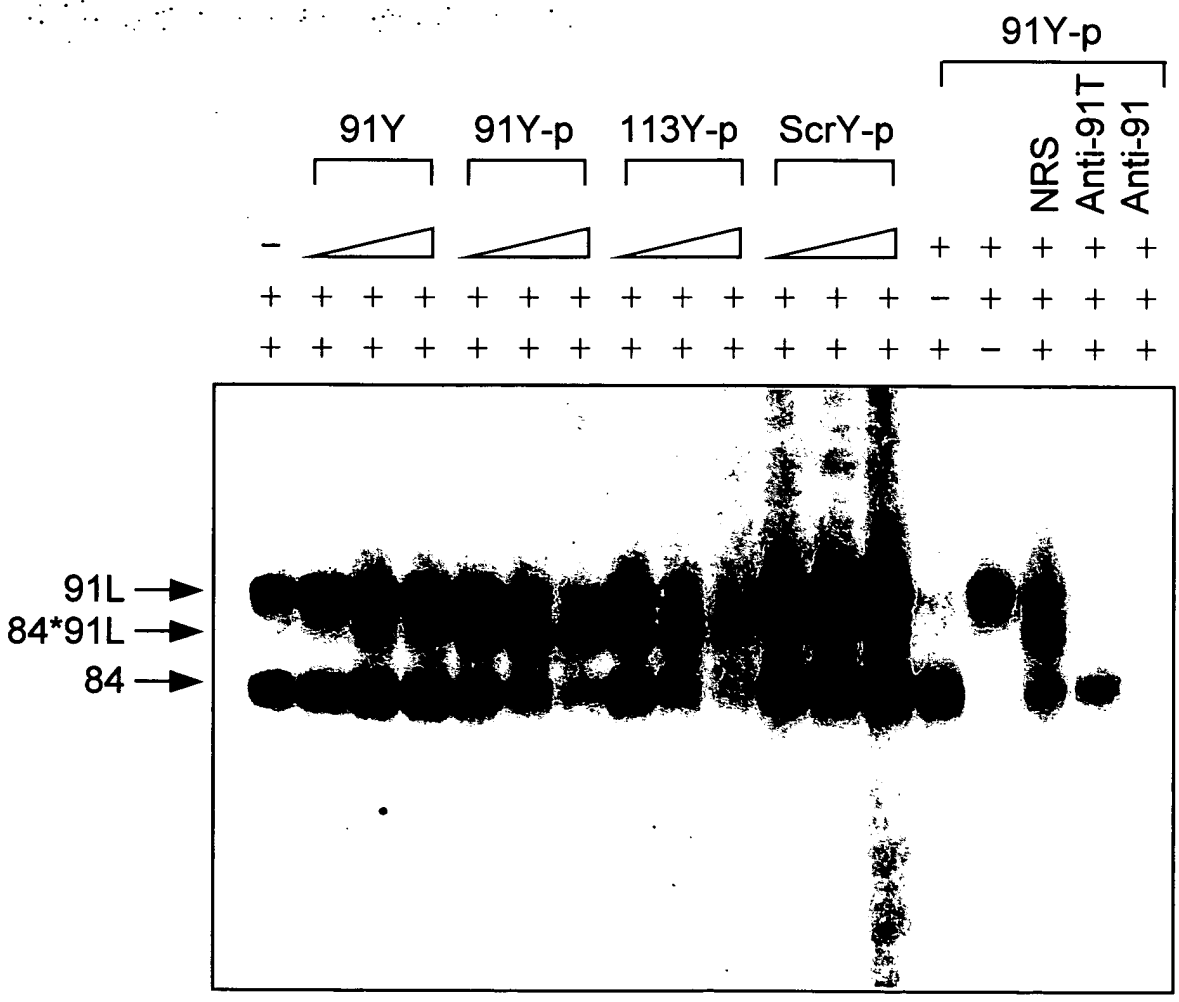

FIG. 22A

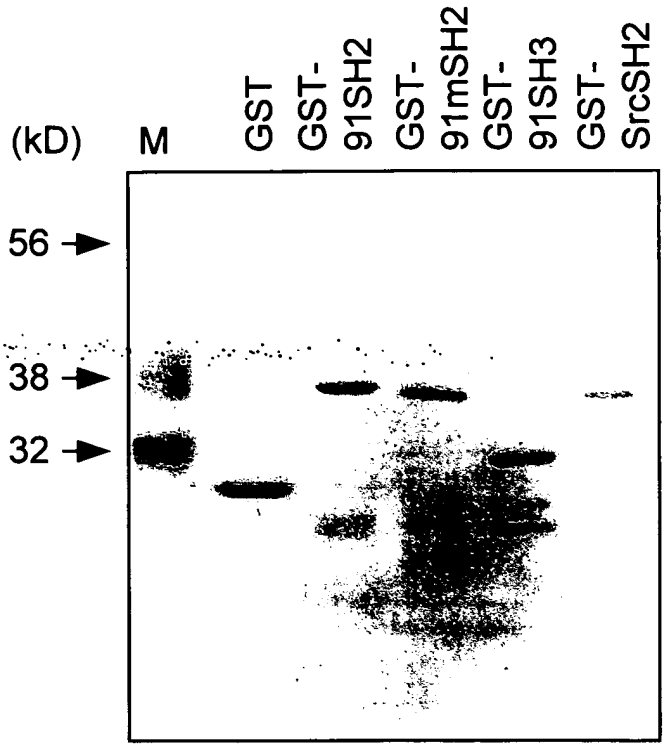

FIG. 22B

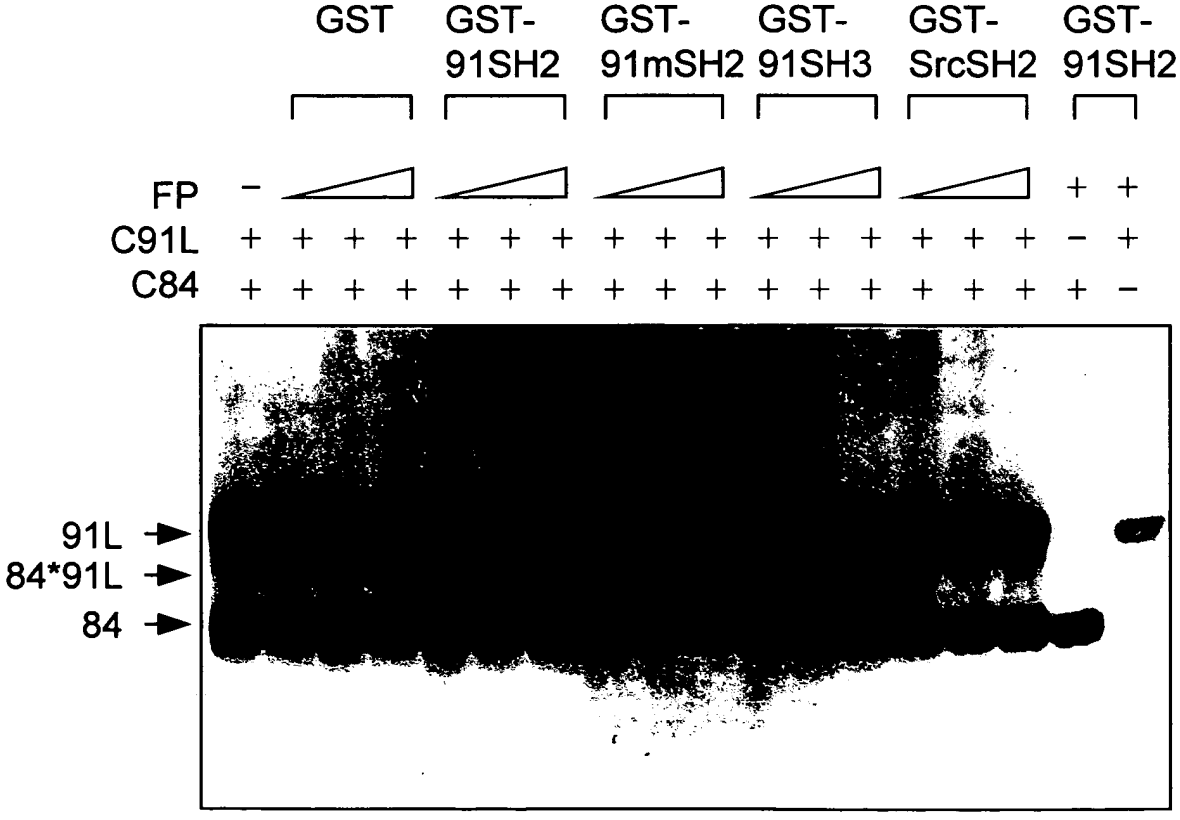

FIG.23A

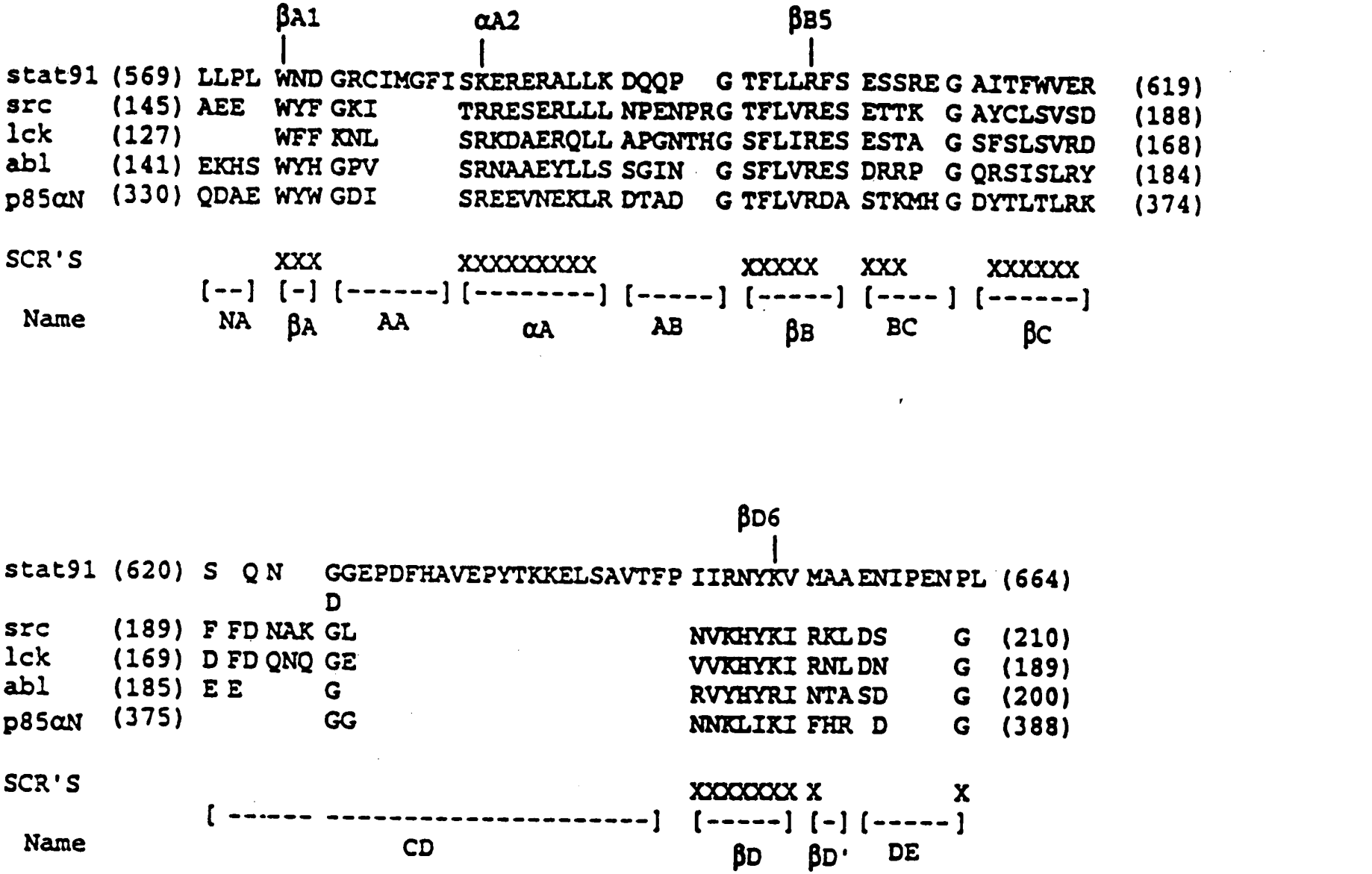

FIG.23B